GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 28, 2003, 18:25:32 ; Search time 5.15152 Seconds
(without alignments)
91.287 Million cell updates/sec

Title: US-09-743-225-7
Perfect score: 55
Sequence: 1 CATLRVYKGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	65.5	367	1	INX4_DROME	Q9vrx6 drosophila
2	35	63.6	244	1	PHOS_MOUSE	Q9qw08 mus musculu
3	35	63.6	245	1	PHOS_BOVIN	P19632 bos taurus
4	35	63.6	245	1	PHOS_FELCA	P41686 felis silve
5	35	63.6	246	1	PHOS_RAT	P20942 rattus norv
6	35	63.6	340	1	CFAA_BACUT	Q45729 bacillus th
7	35	63.6	424	1	VGLI_HSVEB	P18553 equine herp
8	35	63.6	712	1	CDGT_BACS3	P09121 bacillus sp
9	35	63.6	713	1	AMYR_BACS8	P17692 bacillus sp
10	35	63.6	713	1	CDGT_BACSO	P05618 bacillus sp
11	35	63.6	713	1	CDGT_BACSP	P30921 bacillus sp
12	35	63.6	713	1	CDGU_BACCI	P43379 bacillus ci
13	34	61.8	245	1	PHOS_CANFA	O77560 canis famil
14	34	61.8	246	1	PHOS_HUMAN	P20941 homo sapien
15	34	61.8	345	1	APOH_HUMAN	P02749 homo sapien
16	34	61.8	349	1	ADH1_ASPFL	P41747 aspergillus
17	34	61.8	349	1	ADH1_EMENI	P08843 emericella
18	34	61.8	349	1	RADA_PYRFU	O74036 pyrococcus
19	34	61.8	352	1	ADH3_EMENI	P07754 emericella
20	34	61.8	353	1	ADH1_NEUCR	Q9p6c8 neurospora
21	34	61.8	356	1	RADA_PYRAB	Q9v233 pyrococcus
22	34	61.8	529	1	RADA_PYRHO	O58001 pyrococcus
23	34	61.8	633	1	DXS_BACSU	P54523 bacillus su
24	33	60.0	107	1	THIO_STRCL	Q05739 streptomyce
25	33	60.0	110	1	THIO_STRCO	P52230 streptomyce
26	33	60.0	340	1	ADHA_RHIME	O31186 rhizobium m
27	33	60.0	483	1	CORT_DROME	Q960n3 drosophila
28	33	60.0	539	1	DOP2_DROME	Q24563 drosophila
29	33	60.0	638	1	OAR1_LYMST	O77408 lymnaea sta
30	33	60.0	718	1	CDGT_BACCI	P30920 bacillus ci
31	33	60.0	718	1	CDGT_BACLI	P14014 bacillus li
32	33	60.0	718	1	CDGT_BACSS	P31747 bacillus sp
33	33	60.0	849	1	RSG2_HUMAN	Q15283 homo sapien
34	33	60.0	931	1	LUG_ARATH	Q9fuy2 arabidopsis
35	33	60.0	1111	1	MYSB_DICDI	P34092 dictyosteli
36	33	60.0	1240	1	DPOL_HSV21	P07918 herpes simp
37	33	60.0	1435	1	TR85_HUMAN	Q9y215 homo sapien
38	33	60.0	1992	1	TRIB_HUMAN	Q14669 homo sapien
39	32	58.2	298	1	PANE_BACSU	O34661 bacillus su
40	32	58.2	346	1	ANX1_RABIT	P51662 oryctolagus
41	32	58.2	351	1	ARGC_PYRAE	Q8zua0 pyrobaculum
42	32	58.2	419	1	YHAP_BACSU	O07523 bacillus su
43	32	58.2	431	1	URTB_DESRO	P98121 desmodus ro
44	32	58.2	469	1	CISY_FRAAN	P83372 fragaria an
45	32	58.2	477	1	URT2_DESRO	P15638 desmodus ro

ALIGNMENTS

RESULT 1
INX4_DROME
ID INX4_DROME STANDARD; PRT; 367 AA.
AC Q9VRX6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Innexin Inx4 (Innexin-4) (Zero population growth protein).
GN ZPG OR INX4 OR CG10125.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Ovary;
RX MEDLINE=21959302; PubMed=11960713;
RA Stebbings L.A., Todman M.G., Phillips R., Greer C.E., Tam J.,
RA Phelan P., Jacobs K., Bacon J.P., Davies J.A.;
RT "Gap junctions in Drosophila: developmental expression of the entire
RT innexin gene family.";
RL Mech. Dev. 113:197-205(2002).
RN [2]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE=Ovary;
RX PubMed=11973283;
RA Tazuke S.I., Schulz C., Gilboa L., Fogarty M., Mahowald A.P.,
RA Guichet A., Ephrussi A., Wood C.G., Lehmann R., Fuller M.T.;
RT "A germline-specific gap junction protein required for survival of
RT differentiating early germ cells.";
RL Development 129:2529-2539(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

```
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley; TISSUE=Embryo;
RX   MEDLINE=22426066; PubMed=12537569;
RA   Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA   George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA   Rubin G.M., Celniker S.E.;
RT   "A Drosophila full-length cDNA resource.";
RL   Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC   -!- FUNCTION: Structural component of the gap junctions in germ line
CC       cells. Required for differentiation and survival of germline cysts
CC       in females and of spermatogonia in males; gap junctional
CC       communication between spermatogonia and somatic cyst cells may be
CC       required for normal differentiation and survival of spermatogonia.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein; concentrated at
CC       the interface between germline and somatic support cells in
CC       spermatogonia, early spermatocytes and germ cells in the ovary.
CC   -!- TISSUE SPECIFICITY: Expressed in nurse cells and oocyte during
CC       oogenesis. Uniform expression in imaginal wing disk and low
CC       expression in developing imaginal CNS. Expressed in embryonic pole
CC       cells and primordial germ cells.
CC   -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
CC       First seen at the embryonic syncitial blastoderm stage.
CC   -!- SIMILARITY: Belongs to the innexin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF271718; AAL36976.1; -.
DR   EMBL; AE003562; AAF50655.1; -.
DR   EMBL; AY094856; AAM11209.1; -.
DR   FlyBase; FBgn0024177; zpg.
DR   GO; GO:0007281; P:germ-cell development; IMP.
DR   InterPro; IPR000990; Innexin.
DR   Pfam; PF00876; Innexin; 1.
DR   PRINTS; PR01262; INNEXIN.
KW   Gap junction; Transmembrane.
FT   DOMAIN        1     21       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      22    42       POTENTIAL.
FT   DOMAIN        43    110      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      111   131      POTENTIAL.
FT   DOMAIN        132   186      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      187   207      POTENTIAL.
FT   DOMAIN        208   268      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      269   289      POTENTIAL.
FT   DOMAIN        290   367      CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   367 AA;  42784 MW;  B984A4035DA7CF3E CRC64;

  Query Match             65.5%;  Score 36;  DB 1;  Length 367;
  Best Local Similarity   60.0%;  Pred. No. 9.8;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CATLRVYKGG 10
              ||   :|||| .
Db        237 CAKCEMYKGG 246


RESULT 2
PHOS_MOUSE
ID   PHOS_MOUSE     STANDARD;      PRT;   244 AA.
AC   Q9QW08;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Phosducin (PHD) (33 kDa phototransducing protein) (Rod photoreceptor
DE   1) (RPR-1).
GN   PDC OR RPR1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Retina;
RX   MEDLINE=94009395; PubMed=8405193;
RA   Groshan K.R., Norton J.C., Craft C.M., Travis G.H.;
RT   "Isolation and characterization of a cDNA for mouse retinal
RT   phosducin.";
RL   Exp. Eye Res. 57:253-255(1993).
CC   -!- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
CC       PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
CC       METABOLISM.
CC   -!- SUBUNIT: Forms a complex with the beta and gamma subunits of
CC       the GTP-binding protein, transducin.
CC   -!- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
CC   -!- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
CC       MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
CC   -!- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; L08075; AAK13559.1; -.
DR   PIR; JC2018; JC2018.
DR   HSSP; P20942; 1B9X.
DR   MGD; MGI:98090; Pdc.
DR   InterPro; IPR001200; Phosducin.
DR   InterPro; IPR006663; Thioredox_dom2.
DR   Pfam; PF02114; Phosducin; 1.
DR   PRINTS; PR00677; PHOSDUCIN.
KW   Vision; Sensory transduction; Phosphorylation.
FT   MOD_RES       71     71       PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
SQ   SEQUENCE   244 AA;  28016 MW;  F42361EA25F0F254 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 244;
  Best Local Similarity   87.5%;  Pred. No. 10;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TLRVYKGG 10
              || |||||
Db        186 TLLVYKGG 193


RESULT 3
PHOS_BOVIN
ID   PHOS_BOVIN     STANDARD;      PRT;   245 AA.
AC   P19632; P20940; Q28160;
```

```
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein).
GN   PDC.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE, AND SEQUENCE OF 228-245 FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=90368806; PubMed=2203790;
RA   Lee R.H., Fowler A., McGinnis J.F., Lolley R.N., Craft C.M.;
RT   "Amino acid and cDNA sequence of bovine phosducin, a soluble
RT   phosphoprotein from photoreceptor cells.";
RL   J. Biol. Chem. 265:15867-15873(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89364083; PubMed=2770450;
RA   Kuo C.-H., Akiyama M., Miki N.;
RT   "Isolation of a novel retina-specific clone (MEKA cDNA) encoding a
RT   photoreceptor soluble protein.";
RL   Brain Res. Mol. Brain Res. 6:1-10(1989).
RN   [3]
RP   SEQUENCE OF 8-245 FROM N.A.
RC   TISSUE=Pineal gland, and Retina;
RX   MEDLINE=91007277; PubMed=2210381;
RA   Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,
RA   Shinohara T.;
RT   "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in
RT   retina and pineal gland.";
RL   Gene 91:209-215(1990).
RN   [4]
RP   PHOSPHORYLATION OF SER-73.
RX   MEDLINE=90368805; PubMed=2394752;
RA   Lee R.H., Brown B.M., Lolley R.N.;
RT   "Protein kinase A phosphorylates retinal phosducin on serine 73 in
RT   situ.";
RL   J. Biol. Chem. 265:15860-15866(1990).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH G-BETA AND
RP   G-GAMMA.
RX   MEDLINE=98416696; PubMed=9739091;
RA   Loew A., Ho Y.K., Blundell T., Bax B.;
RT   "Phosducin induces a structural change in transducin beta gamma.";
RL   Structure 6:1007-1019(1998).
CC   -!- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
CC       PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
CC       METABOLISM.
CC   -!- SUBUNIT: Forms a complex with the beta and gamma subunits of
CC       the GTP-binding protein, transducin.
CC   -!- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
CC   -!- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
CC       MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
CC   -!- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
CC   -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS
CC       DUE TO A FRAMESHIFT.
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CC   ---------------------------------------------------------------------
DR   EMBL; M58170; AAA62716.1; -.
DR   EMBL; M33529; AAA30349.1; -.
DR   PIR; A38379; A38379.
DR   PDB; 1A0R; 16-FEB-99.
DR   InterPro; IPR001200; Phosducin.
DR   InterPro; IPR006663; Thioredox_dom2.
DR   Pfam; PF02114; Phosducin; 1.
DR   PRINTS; PR00677; PHOSDUCIN.
KW   Vision; Sensory transduction; Phosphorylation; 3D-structure.
FT   MOD_RES      73     73       PHOSPHORYLATION (BY PKA).
FT   CONFLICT     44     44       H -> P (IN REF. 3).
FT   CONFLICT    238    239       TN -> SK (IN REF. 3).
FT   HELIX        21     35
FT   TURN         36     36
FT   HELIX        74     80
FT   TURN         81     82
FT   HELIX        87    105
FT   STRAND      114    116
FT   HELIX       120    128
FT   TURN        132    133
FT   STRAND      135    141
FT   TURN        143    144
FT   TURN        146    147
FT   HELIX       148    161
FT   TURN        163    164
FT   STRAND      166    171
FT   HELIX       172    175
FT   TURN        178    179
FT   TURN        183    185
FT   STRAND      188    193
FT   TURN        194    195
FT   STRAND      196    201
FT   TURN        202    203
FT   HELIX       204    207
FT   TURN        210    211
FT   HELIX       214    222
FT   TURN        223    225
SQ   SEQUENCE   245 AA;  28231 MW;  5CA621610401D550 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 245;
  Best Local Similarity   87.5%;  Pred. No. 10;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TLRVYKGG 10
              || |||||
Db        188 TLLVYKGG 195


RESULT 4
PHOS_FELCA
ID   PHOS_FELCA     STANDARD;      PRT;   245 AA.
AC   P41686;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosducin (PHD) (33 kDa phototransducing protein).
GN   PDC.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Abyssinian; TISSUE=Retina;
RX   MEDLINE=95178554; PubMed=7873608;
RA   Gorin M.B., To A.C., Narfstrom K.;
RT   "Sequence analysis and exclusion of phosducin as the gene for the
RT   recessive retinal degeneration of the Abyssinian cat.";
RL   Biochim. Biophys. Acta 1260:323-327(1995).
CC   -!- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
CC       PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
CC       METABOLISM.
CC   -!- SUBUNIT: Forms a complex with the beta and gamma subunits of
CC       the GTP-binding protein, transducin.
CC   -!- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS
CC       (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L35314; AAB59257.1; -.
DR   PIR; S52096; S52096.
DR   HSSP; P20942; 1B9X.
DR   InterPro; IPR001200; Phosducin.
DR   InterPro; IPR006663; Thioredox_dom2.
DR   Pfam; PF02114; Phosducin; 1.
DR   PRINTS; PR00677; PHOSDUCIN.
KW   Vision; Sensory transduction; Phosphorylation.
FT   MOD_RES      73     73       PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
SQ   SEQUENCE   245 AA;  28363 MW;  9807CD30C32F8B21 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 245;
  Best Local Similarity   87.5%;  Pred. No. 10;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TLRVYKGG 10
              || |||||
Db        188 TLLVYKGG 195


RESULT 5
PHOS_RAT
ID   PHOS_RAT       STANDARD;      PRT;   246 AA.
AC   P20942; Q63420;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein) (Rod
DE   photoreceptor 1) (RPR-1).
GN   PDC OR RPR1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Pineal gland, and Retina;
RX   MEDLINE=91007277; PubMed=2210381;
RA   Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,
RA   Shinohara T.;
RT   "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in
RT   retina and pineal gland.";
RL   Gene 91:209-215(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pineal gland;
RX   MEDLINE=91301696; PubMed=2071146;
RA   Craft C.M., Lolley R.N., Seldin M.F., Lee R.H.;
RT   "Rat pineal gland phosducin: cDNA isolation, nucleotide sequence, and
RT   chromosomal assignment in the mouse.";
RL   Genomics 10:400-409(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH G-BETA AND
RP   G-GAMMA.
RX   MEDLINE=99288453; PubMed=10360181;
RA   Gaudet R., Savage J.R., McLaughlin J.N., Willardson B.M., Sigler P.B.;
RT   "A molecular mechanism for the phosphorylation-dependent regulation of
RT   heterotrimeric G-proteins by phosducin. Structural analysis of
RT   phosducin and its phosphorylation-regulated interaction with
RT   transducin beta-gamma.";
RL   Mol. Cell 3:649-660(1999).
CC   -!- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
CC       PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
CC       METABOLISM.
CC   -!- SUBUNIT: Forms a complex with the beta and gamma subunits of
CC       the GTP-binding protein, transducin.
CC   -!- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
CC   -!- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
CC       MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
CC   -!- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M33528; AAA40604.1; -.
DR   EMBL; M33530; AAA40603.1; -.
DR   EMBL; M60738; AAA41841.1; -.
DR   PIR; A39903; A39903.
DR   PIR; JH0216; JH0216.
DR   PDB; 1B9X; 23-FEB-99.
DR   PDB; 1B9Y; 23-FEB-99.
DR   PDB; 2TRC; 05-JUN-97.
DR   InterPro; IPR001200; Phosducin.
DR   InterPro; IPR006663; Thioredox_dom2.
DR   Pfam; PF02114; Phosducin; 1.
DR   PRINTS; PR00677; PHOSDUCIN.
KW   Vision; Sensory transduction; Phosphorylation; 3D-structure.
FT   MOD_RES      73     73       PHOSPHORYLATION (BY PKA).
FT   VARIANT     191    191       V -> I.
FT   CONFLICT     39     39       G -> S (IN REF. 2).
FT   CONFLICT     88     88       G -> V (IN REF. 2).
FT   CONFLICT    119    119       T -> S (IN REF. 2).
FT   CONFLICT    211    211       D -> E (IN REF. 2).
FT   HELIX        21     36
FT   TURN         37     37
FT   HELIX        88    105
FT   STRAND      114    116
FT   HELIX       120    128
FT   TURN        132    133
FT   STRAND      135    141
FT   TURN        143    144
FT   TURN        146    147
FT   HELIX       148    161
FT   TURN        163    164
FT   STRAND      166    171
FT   HELIX       172    175
FT   TURN        176    176
FT   TURN        178    180
FT   TURN        183    185
FT   STRAND      188    193
FT   TURN        194    195
FT   STRAND      196    201
FT   TURN        202    203
FT   HELIX       204    207
FT   HELIX       214    222
FT   TURN        223    225
SQ   SEQUENCE   246 AA;  28129 MW;  3C48ABCB4E5E3D04 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 246;
  Best Local Similarity   87.5%;  Pred. No. 10;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TLRVYKGG 10
              || |||||
Db        188 TLLVYKGG 195


RESULT 6
CFAA_BACUT
ID   CFAA_BACUT     STANDARD;      PRT;   340 AA.
AC   Q45729;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
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DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Pesticidial crystal protein cry15Aa (Insecticidal delta-endotoxin
DE   CryXVA(a)) (Crystaline entomocidal protoxin) (38 kDa crystal
DE   protein).
GN   CRY15AA OR CRYXVA(A).
OS   Bacillus thuringiensis (subsp. thompsoni).
OG   Plasmid.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=44162;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92105024; PubMed=1729243;
RA   Brown K.L., Whiteley H.R.;
RT   "Molecular characterization of two novel crystal protein genes from
RT   Bacillus thuringiensis subsp. thompsoni.";
RL   J. Bacteriol. 174:549-557(1992).
CC   -!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC       EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE.
CC   -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC       SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC       OF THE SPORE COAT.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M76442; AAA22333.1; -.
DR   PIR; B41969; B41969.
DR   InterPro; IPR005831; Aer_hem.
KW   Toxin; Sporulation; Plasmid.
SQ   SEQUENCE   340 AA;  37547 MW;  BCBFA24FE9B1FA50 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 340;
  Best Local Similarity   75.0%;  Pred. No. 14;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ATLRVYKG 9
              |||::|||
Db        160 ATLQIYKG 167


RESULT 7
VGLI_HSVEB
ID   VGLI_HSVEB     STANDARD;      PRT;   424 AA.
AC   P18553;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Glycoprotein I precursor.
GN   GI OR 73.
OS   Equine herpesvirus type 1 (strain Ab4p) (EHV-1),
OS   Equine herpesvirus type 1 (strain AB1) (EHV-1), and
OS   Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Varicellovirus.
OX   NCBI_TaxID=31520, 10328, 10330;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AB4P;
RX   MEDLINE=92295566; PubMed=1318606;
RA   Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT   "The DNA sequence of equine herpesvirus-1.";
RL   Virology 189:304-316(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AB1;
RX   MEDLINE=91276272; PubMed=1647359;
RA   Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
RA   Bonass W.A.;
RT   "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine
RT   herpesvirus type-1 short unique region.";
RL   Gene 101:203-208(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Kentucky D;
RX   MEDLINE=91108393; PubMed=2177089;
RA   Audonnet J.-C., Winslow J., Allen G., Paoletti E.;
RT   "Equine herpesvirus type 1 unique short fragment encodes
RT   glycoproteins with homology to herpes simplex virus type 1 gD, gI and
RT   gE.";
RL   J. Gen. Virol. 71:2969-2978(1990).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GPIV,
CC       AND TO PRV GP63.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86664; AAB02508.1; -.
DR   EMBL; M36299; AAA66547.1; -.
DR   PIR; C36646; VGBEE9.
DR   InterPro; IPR002874; Herpes_gI.
DR   Pfam; PF01688; Herpes_gI; 1.
KW   Glycoprotein; Signal; Transmembrane.
FT   SIGNAL       1     22       POTENTIAL.
FT   CHAIN       23    424       GLYCOPROTEIN I.
FT   DOMAIN      23    319       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    320   340       POTENTIAL.
FT   DOMAIN      341   424       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     35    35       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     67    67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     78    78       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    121   121       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    131   131       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    236   236       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    307   307       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   424 AA;  46392 MW;  EE9BEF7DAA895806 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 424;
  Best Local Similarity   50.0%;  Pred. No. 18;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATLRVYKGG 10
              ||: |:|: |
Db        351 CASRRIYRSG 360


RESULT 8
CDGT_BACS3
ID   CDGT_BACS3     STANDARD;      PRT;   712 AA.
AC   P09121;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE   (Cyclodextrin-glycosyltransferase) (CGTase).
GN   CGT.
OS   Bacillus sp. (strain 38-2).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1412;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
RX   MEDLINE=89036108; PubMed=2972812;
RA   Kaneko T., Hamamoto T., Horikoshi K.;
RT   "Molecular cloning and nucleotide sequence of the cyclomaltodextrin
RT   glucanotransferase gene from the alkalophilic Bacillus sp. strain no.
RT   38-2.";
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RL   J. Gen. Microbiol. 134:97-105(1988).
RN   [2]
RP   SEQUENCE OF 1-586 FROM N.A.
RA   Hamamoto T., Kaneko T., Horikoshi K.;
RT   "Nucleotide sequence of the cyclomaltodextrin glucanotransferase
RT   (CGTase) gene from alkalophilic Bacillus sp. strain No. 38-2.";
RL   Agric. Biol. Chem. 51:2019-2022(1987).
CC   -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC       of a 1,4-alpha-D-glucosidic bond.
CC   -!- COFACTOR: BINDS TWO CALCIUM IONS.
CC   -!- SUBUNIT: Monomer.
CC   -!- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC       IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC       IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC       ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC       ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC       MALTOOLIGOSACCHARIDE PRODUCED.
CC   -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC       KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M19880; AAA22309.1; -.
DR   EMBL; D00129; BAA00077.1; -.
DR   HSSP; P05618; 1PAM.
DR   InterPro; IPR006589; Alp_amyl_cat_sub.
DR   InterPro; IPR006048; Alpha_amyl_C.
DR   InterPro; IPR006047; Alpha_amyl_cat.
DR   InterPro; IPR002044; CBD_4.
DR   InterPro; IPR006046; Glyco_hydro_13.
DR   InterPro; IPR002909; IPT_TIG.
DR   Pfam; PF00128; alpha-amylase; 1.
DR   Pfam; PF02806; alpha-amylase_C; 1.
DR   Pfam; PF00686; CBM_20; 1.
DR   Pfam; PF01833; TIG; 1.
DR   PRINTS; PR00110; ALPHAAMYLASE.
DR   ProDom; PD001568; CBD_4; 1.
DR   SMART; SM00642; Aamy; 1.
DR   SMART; SM00632; Aamy_C; 1.
KW   Transferase; Glycosyltransferase; Calcium; Signal.
FT   SIGNAL        1     27
FT   CHAIN        28    712       CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT   DOMAIN       28    165       A1.
FT   DOMAIN      166    229       B.
FT   DOMAIN      230    433       A2.
FT   DOMAIN      434    522       C.
FT   DOMAIN      523    608       D.
FT   DOMAIN      609    712       E.
FT   DISULFID     70     77       BY SIMILARITY.
FT   ACT_SITE    256    256       BY SIMILARITY.
FT   ACT_SITE    284    284       BY SIMILARITY.
FT   ACT_SITE    355    355       BY SIMILARITY.
FT   CONFLICT    582    586       VPGGI -> SWRHL (IN REF. 2).
SQ   SEQUENCE   712 AA;  78249 MW;  4FAA8F70BEF818F9 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 712;
  Best Local Similarity   60.0%;  Pred. No. 30;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CATLRVYKGG 10
              |  ||:| ||
Db         70 CTNLRLYCGG 79


RESULT 9
AMYR_BACS8
ID   AMYR_BACS8     STANDARD;      PRT;   713 AA.
AC   P17692;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Raw-starch-digesting amylase precursor (EC 3.2.1.1) (1,4-alpha-D-
DE   glucan glucanohydrolase).
OS   Bacillus sp. (strain B1018).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1417;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
RX   MEDLINE=90147765; PubMed=1689153;
RA   Itkor P., Tsukagoshi N., Udaka S.;
RT   "Nucleotide sequence of the raw-starch-digesting amylase gene from
RT   Bacillus sp. B1018 and its strong homology to the cyclodextrin
RT   glucanotransferase genes.";
RL   Biochem. Biophys. Res. Commun. 166:630-636(1990).
CC   -!- FUNCTION: THIS ENDO-TYPE ADSORBABLE AMYLASE IS CAPABLE TO
CC       DIGEST RAW-STARCH.
CC   -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC       linkages in oligosaccharides and polysaccharides.
CC   -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC       KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M33302; AAA22239.1; -.
DR   EMBL; D90112; BAA14140.1; -.
DR   PIR; S09196; S09196.
DR   HSSP; P43379; 1CDG.
DR   InterPro; IPR006589; Alp_amyl_cat_sub.
DR   InterPro; IPR006048; Alpha_amyl_C.
DR   InterPro; IPR006047; Alpha_amyl_cat.
DR   InterPro; IPR002044; CBD_4.
DR   InterPro; IPR006046; Glyco_hydro_13.
DR   InterPro; IPR002909; IPT_TIG.
DR   Pfam; PF00128; alpha-amylase; 1.
DR   Pfam; PF02806; alpha-amylase_C; 1.
DR   Pfam; PF00686; CBM_20; 1.
DR   Pfam; PF01833; TIG; 1.
DR   PRINTS; PR00110; ALPHAAMYLASE.
DR   ProDom; PD001568; CBD_4; 1.
DR   SMART; SM00642; Aamy; 1.
DR   SMART; SM00632; Aamy_C; 1.
KW   Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal.
FT   SIGNAL        1     27
FT   CHAIN        28    713       RAW-STARCH-DIGESTING AMYLASE.
FT   ACT_SITE    256    256       BY SIMILARITY.
FT   ACT_SITE    260    260       BY SIMILARITY.
FT   ACT_SITE    355    355       BY SIMILARITY.
SQ   SEQUENCE   713 AA;  77420 MW;  85FB616DA687B888 CRC64;

  Query Match             63.6%;  Score 35;  DB 1;  Length 713;
  Best Local Similarity   60.0%;  Pred. No. 30;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CATLRVYKGG 10
              |  ||:| ||
Db         70 CTNLRLYCGG 79


RESULT 10
CDGT_BACS0
ID   CDGT_BACS0     STANDARD;      PRT;   713 AA.
AC   P05618;
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DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE   (Cyclodextrin-glycosyltransferase) (CGTase).
GN   CGT.
OS   Bacillus sp. (strain 1011).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1410;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87308036; PubMed=2957361;
RA   Kimura K., Kataoka S., Ishii Y., Takano T., Yamane K.;
RT   "Nucleotide sequence of the beta-cyclodextrin glucanotransferase gene
RT   of alkalophilic Bacillus sp. strain 1011 and similarity of its amino
RT   acid sequence to those of alpha-amylases.";
RL   J. Bacteriol. 169:4399-4402(1987).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RA   Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
RT   "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
RT   Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A
RT   resolution.";
RL   Acta Crystallogr. D 52:1136-1145(1996).
CC   -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC       of a 1,4-alpha-D-glucosidic bond.
CC   -!- COFACTOR: BINDS TWO CALCIUM IONS.
CC   -!- SUBUNIT: Monomer.
CC   -!- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC       IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC       IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC       ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC       ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC       MALTOOLIGOSACCHARIDE PRODUCED.
CC   -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC       KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M17366; AAA22308.1; -.
DR   PIR; A26678; ALBSG1.
DR   PDB; 1PAM; 11-JAN-97.
DR   PDB; 1D7F; 17-MAR-00.
DR   PDB; 1DED; 07-APR-00.
DR   PDB; 1I75; 11-APR-01.
DR   InterPro; IPR006589; Alp_amyl_cat_sub.
DR   InterPro; IPR006048; Alpha_amyl_C.
DR   InterPro; IPR006047; Alpha_amyl_cat.
DR   InterPro; IPR002044; CBD_4.
DR   InterPro; IPR006046; Glyco_hydro_13.
DR   InterPro; IPR002909; IPT_TIG.
DR   Pfam; PF00128; alpha-amylase; 1.
DR   Pfam; PF02806; alpha-amylase_C; 1.
DR   Pfam; PF00686; CBM_20; 1.
DR   Pfam; PF01833; TIG; 1.
DR   PRINTS; PR00110; ALPHAAMYLASE.
DR   ProDom; PD001568; CBD_4; 1.
DR   SMART; SM00642; Aamy; 1.
DR   SMART; SM00632; Aamy_C; 1.
KW   Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
FT   SIGNAL       1     27
FT   CHAIN       28    713       CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT   DOMAIN      28    165       A1.
FT   DOMAIN     166    229       B.
FT   DOMAIN     230    433       A2.
FT   DOMAIN     434    522       C.
FT   DOMAIN     523    609       D.
FT   DOMAIN     610    713       E.
FT   DISULFID    70     77       BY SIMILARITY.
FT   ACT_SITE   256    256       BY SIMILARITY.
FT   ACT_SITE   284    284       BY SIMILARITY.
FT   ACT_SITE   355    355       BY SIMILARITY.
FT   TURN        30     31
FT   TURN        33     34
FT   TURN        40     41
FT   STRAND      44     46
FT   HELIX       49     51
FT   TURN        52     52
FT   HELIX       57     59
FT   HELIX       63     65
FT   STRAND      66     66
FT   TURN        68     69
FT   TURN        73     74
FT   STRAND      76     76
FT   HELIX       81     89
FT   TURN        90     93
FT   HELIX       94     96
FT   TURN        97     97
FT   STRAND     100    103
FT   STRAND     107    109
FT   STRAND     114    116
FT   TURN       117    118
FT   STRAND     119    121
FT   TURN       124    125
FT   STRAND     129    135
FT   TURN       137    139
FT   HELIX      142    154
FT   TURN       155    156
FT   STRAND     158    163
FT   TURN       165    166
FT   STRAND     167    170
FT   TURN       176    177
FT   TURN       179    182
FT   STRAND     184    186
FT   TURN       187    188
FT   STRAND     189    192
FT   TURN       195    196
FT   TURN       198    199
FT   STRAND     202    202
FT   STRAND     207    207
FT   HELIX      213    218
FT   STRAND     220    220
FT   TURN       222    223
FT   STRAND     224    227
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FT   HELIX      232    247
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FT   TURN       256    257
FT   HELIX      258    260
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FT   STRAND     280    283
FT   TURN       289    290
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FT   TURN       321    322
FT   HELIX      327    340
FT   TURN       342    343
FT   HELIX      344    346
FT   STRAND     348    349
FT   TURN       354    355
FT   TURN       362    363
FT   HELIX      366    378
FT   STRAND     382    386
FT   TURN       387    388
FT   HELIX      389    391
FT   TURN       392    392
FT   TURN       398    399
FT   HELIX      400    402
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FT   HELIX       413    421
FT   TURN        422    423
FT   HELIX       424    427
FT   HELIX       429    433
FT   STRAND      435    441
FT   STRAND      445    452
FT   TURN        453    454
FT   STRAND      455    462
FT   STRAND      469    471
FT   STRAND      475    475
FT   STRAND      481    483
FT   TURN        486    491
FT   STRAND      496    498
FT   HELIX       500    502
FT   STRAND      503    504
FT   STRAND      507    509
FT   TURN        511    512
FT   STRAND      514    519
FT   STRAND      527    532
FT   STRAND      535    536
FT   TURN        538    539
FT   STRAND      541    547
FT   STRAND      555    558
FT   TURN        559    560
FT   STRAND      561    563
FT   HELIX       565    567
FT   STRAND      568    571
FT   STRAND      575    579
FT   STRAND      586    593
FT   TURN        595    596
FT   STRAND      599    599
FT   STRAND      603    608
FT   STRAND      613    621
FT   TURN        627    628
FT   STRAND      630    635
FT   HELIX       638    640
FT   TURN        641    643
FT   HELIX       645    647
FT   STRAND      649    649
FT   STRAND      653    653
FT   TURN        660    661
FT   STRAND      663    670
FT   TURN        671    672
FT   STRAND      674    683
FT   TURN        684    685
FT   STRAND      686    689
FT   STRAND      695    698
FT   STRAND      704    710
SQ   SEQUENCE   713 AA;  78340 MW;  524B259526B56C52 CRC64;

  Query Match           63.6%;  Score 35;  DB 1;  Length 713;
  Best Local Similarity  60.0%;  Pred. No. 30;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CATLRVYKGG 10
              |  ||:| ||
Db         70 CTNLRLYCGG 79


RESULT 11
CDGT_BACSP
ID   CDGT_BACSP     STANDARD;      PRT;   713 AA.
AC   P30921;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   01-JUL-1993 (Rel. 26, Last annotation update)
DE   Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE   (Cyclodextrin-glycosyltransferase) (CGTase).
GN   CGT.
OS   Bacillus sp. (strain 17-1).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1409;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
RX   MEDLINE=90257592; PubMed=2534600;
RA   Kaneko T., Song K.B., Hamamoto T., Kudo T., Horikoshi K.;
RT   "Construction of a chimeric series of Bacillus cyclomaltodextrin
RT   glucanotransferases and analysis of the thermal stabilities and pH
RT   optima of the enzymes.";
RL   J. Gen. Microbiol. 135:3447-3457(1989).
CC   -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC       of a 1,4-alpha-D-glucosidic bond.
CC   -!- COFACTOR: BINDS TWO CALCIUM IONS.
CC   -!- SUBUNIT: Monomer.
CC   -!- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC       IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC       IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC       ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC       ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC       MALTOOLIGOSACCHARIDE PRODUCED.
CC   -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC       KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M28053; AAA22310.1; -.
DR   HSSP; P43379; 1CDG.
DR   InterPro; IPR006589; Alp_amyl_cat_sub.
DR   InterPro; IPR006048; Alpha_amyl_C.
DR   InterPro; IPR006047; Alpha_amyl_cat.
DR   InterPro; IPR002044; CBD_4.
DR   InterPro; IPR002909; IPT_TIG.
DR   Pfam; PF00128; alpha-amylase; 1.
DR   Pfam; PF02806; alpha-amylase_C; 1.
DR   Pfam; PF00686; CBM_20; 1.
DR   Pfam; PF01833; TIG; 1.
DR   ProDom; PD001568; CBD_4; 1.
DR   SMART; SM00642; Aamy; 1.
DR   SMART; SM00632; Aamy_C; 1.
KW   Transferase; Glycosyltransferase; Calcium; Signal.
FT   SIGNAL        1     27
FT   CHAIN        28    713       CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT   DOMAIN       28    165       A1.
FT   DOMAIN      166    229       B.
FT   DOMAIN      230    433       A2.
FT   DOMAIN      434    522       C.
FT   DOMAIN      523    609       D.
FT   DOMAIN      610    713       E.
FT   DISULFID     70     77       BY SIMILARITY.
FT   ACT_SITE    256    256       BY SIMILARITY.
FT   ACT_SITE    284    284       BY SIMILARITY.
FT   ACT_SITE    355    355       BY SIMILARITY.
SQ   SEQUENCE   713 AA;  77389 MW;  D13AEF6C507FF45E CRC64;

  Query Match           63.6%;  Score 35;  DB 1;  Length 713;
  Best Local Similarity  60.0%;  Pred. No. 30;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CATLRVYKGG 10
              |  ||:| ||
Db         70 CTNLRLYCGG 79


RESULT 12
CDGU_BACCI
ID   CDGU_BACCI     STANDARD;      PRT;   713 AA.
AC   P43379;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
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DE   Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE   (Cyclodextrin-glycosyltransferase) (CGTase).
OS   Bacillus circulans.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1397;
RN   [1]
RP   SEQUENCE FROM N.A., SEQUENCE OF 28-37, AND X-RAY CRYSTALLOGRAPHY (2.0
RP   ANGSTROMS).
RC   STRAIN=251;
RX   MEDLINE=94149761; PubMed=8107143;
RA   Lawson C.L., van Montfort R., Strokopytov B., Rozeboom H.J.,
RA   Kalk K.H., de Vries G.E., Penninga D., Dijkhuizen L., Dijkstra B.W.;
RT   "Nucleotide sequence and X-ray structure of cyclodextrin
RT   glycosyltransferase from Bacillus circulans strain 251 in a maltose-
RT   dependent crystal form.";
RL   J. Mol. Biol. 236:590-600(1994).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC   STRAIN=251;
RX   MEDLINE=96094317; PubMed=7493956;
RA   Knegtel R.M.A., Strokopytov B., Penninga D., Faber O.G.,
RA   Rozeboom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.;
RT   "Crystallographic studies of the interaction of cyclodextrin
RT   glycosyltransferase from Bacillus circulans strain 251 with natural
RT   substrates and products.";
RL   J. Biol. Chem. 270:29256-29264(1995).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=97115811; PubMed=8955113;
RA   Penninga D., van der Veen B.A., Knegtel R.M., van Hijum S.A.,
RA   Rozeboom H.J., Kalk K.H., Dijkstra B.W., Dijkhuizen L.;
RT   "The raw starch binding domain of cyclodextrin glycosyltransferase
RT   from Bacillus circulans strain 251.";
RL   J. Biol. Chem. 271:32777-32784(1996).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR.
RC   STRAIN=251;
RX   MEDLINE=96264806; PubMed=8672460;
RA   Strokopytov B., Knegtel R.M.A., Penninga D., Rozeboom H.J., Kalk K.H.,
RA   Dijkhuizen L., Dijkstra B.W.;
RT   "Structure of cyclodextrin glycosyltransferase complexed with a
RT   maltononaose inhibitor at 2.6-A resolution. Implications for product
RT   specificity.";
RL   Biochemistry 35:4241-4249(1996).
CC   -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC       of a 1,4-alpha-D-glucosidic bond.
CC   -!- COFACTOR: Binds two calcium ions.
CC   -!- SUBUNIT: Monomer.
CC   -!- DOMAIN: May consist of two protein domains: the one in the amino-
CC       terminal side cleaves the alpha-1,4-glucosidic bond in starch, and
CC       the other in the C-terminal side catalyzes other activities,
CC       including the reconstitution of an alpha-1,4-glucosidic linkage
CC       for cyclizing the maltooligosaccharide produced.
CC   -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC       KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X78145; CAA55023.1; -.
DR   PIR; A58800; A58800.
DR   PDB; 2CXG; 14-OCT-98.
DR   PDB; 1CDG; 08-MAR-95.
DR   PDB; 1CGV; 27-FEB-95.
DR   PDB; 1CGW; 27-FEB-95.
DR   PDB; 1CGX; 07-FEB-95.
DR   PDB; 1CGY; 07-FEB-95.
DR   PDB; 1CXE; 15-DEC-95.
DR   PDB; 1CXF; 15-DEC-95.
DR   PDB; 1CXH; 15-DEC-95.
DR   PDB; 1CXI; 15-DEC-95.
DR   PDB; 2DIJ; 13-JAN-99.
DR   PDB; 1TCM; 21-APR-97.
DR   PDB; 1CXK; 07-FEB-00.
DR   PDB; 1CXL; 03-SEP-99.
DR   PDB; 1D3C; 22-DEC-99.
DR   PDB; 1DTU; 06-MAR-00.
DR   PDB; 1EO5; 22-NOV-00.
DR   PDB; 1EO7; 22-NOV-00.
DR   PDB; 1KCK; 16-JAN-02.
DR   PDB; 1KCL; 16-JAN-02.
DR   InterPro; IPR006589; Alp_amyl_cat_sub.
DR   InterPro; IPR006048; Alpha_amyl_C.
DR   InterPro; IPR006047; Alpha_amyl_cat.
DR   InterPro; IPR002044; CBD_4.
DR   InterPro; IPR006046; Glyco_hydro_13.
DR   InterPro; IPR002909; IPT_TIG.
DR   Pfam; PF00128; alpha-amylase; 1.
DR   Pfam; PF02806; alpha-amylase_C; 1.
DR   Pfam; PF00686; CBM_20; 1.
DR   Pfam; PF01833; TIG; 1.
DR   PRINTS; PR00110; ALPHAAMYLASE.
DR   ProDom; PD001568; CBD_4; 1.
DR   SMART; SM00642; Aamy; 1.
DR   SMART; SM00632; Aamy_C; 1.
KW   Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
FT   SIGNAL       1    27
FT   CHAIN       28   713       CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT   DOMAIN      28   165       A1.
FT   DOMAIN     166   229       B.
FT   DOMAIN     230   433       A2.
FT   DOMAIN     434   522       C.
FT   DOMAIN     523   609       D.
FT   DOMAIN     610   713       E.
FT   DISULFID    70    77
FT   ACT_SITE   256   256       NUCLEOPHILE.
FT   ACT_SITE   284   284       PROTON DONOR.
FT   ACT_SITE   355   355       SUBSTRATE BINDING.
FT   TURN        30    31
FT   TURN        33    34
FT   TURN        36    37
FT   TURN        40    41
FT   STRAND      44    46
FT   HELIX       49    52
FT   HELIX       57    59
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FT   STRAND      66    66
FT   TURN        68    69
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FT   HELIX       81    89
FT   TURN        90    91
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FT   STRAND     100   103
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FT   STRAND     114   116
FT   TURN       117   118
FT   STRAND     119   121
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FT   STRAND     129   135
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FT   HELIX      142   154
FT   TURN       155   156
FT   STRAND     158   163
FT   TURN       165   166
FT   STRAND     167   170
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FT   STRAND     184   186
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FT   TURN        187    188
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FT   TURN        195    196
FT   STRAND      202    202
FT   STRAND      207    207
FT   HELIX       213    218
FT   STRAND      220    220
FT   TURN        222    223
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FT   HELIX       310    320
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FT   TURN        342    343
FT   HELIX       344    346
FT   STRAND      348    349
FT   TURN        354    355
FT   TURN        362    363
FT   HELIX       366    378
FT   STRAND      382    386
FT   TURN        387    388
FT   HELIX       389    391
FT   TURN        392    392
FT   TURN        398    399
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FT   TURN        422    423
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FT   HELIX       429    433
FT   STRAND      435    441
FT   STRAND      445    451
FT   STRAND      455    462
FT   STRAND      469    471
FT   STRAND      475    475
FT   STRAND      481    483
FT   TURN        486    491
FT   STRAND      496    498
FT   HELIX       500    502
FT   STRAND      503    504

  Query Match             63.6%;  Score 35;  DB 1;  Length 713;
  Best Local Similarity   60.0%;  Pred. No. 30;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CATLRVYKGG 10
              |  ||:| ||
Db         70 CTNLRLYCGG 79


RESULT 13
PHOS_CANFA
ID   PHOS_CANFA     STANDARD;      PRT;   245 AA.
AC   O77560;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosducin (PHD) (33 kDa phototransducing protein).
GN   PDC.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT PD GLY-82.
RX   MEDLINE=98382516; PubMed=9714819;
RA   Zhang Q., Acland G.M., Parshall C.J., Haskell J., Ray K.,
RA   Aguirre G.D.;
RT   "Characterization of canine photoreceptor phosducin cDNA and
RT   identification of a sequence variant in dogs with photoreceptor
RT   dysplasia.";
RL   Gene 215:231-239(1998).
CC   -!- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
CC       PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
CC       METABOLISM.
CC   -!- SUBUNIT: Forms a complex with the beta and gamma subunits of
CC       the GTP-binding protein, transducin.
CC   -!- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS
CC       (BY SIMILARITY).
CC   -!- DISEASE: DEFECTS IN PDC ARE THE CAUSE OF PHOTORECEPTOR DYSPLASIA
CC       (PD); AN AUTOSOMAL RECESSIVE DISEASE OF MINIATURE SCHNAUZER DOGS
CC       CAUSING RETINAL DEGENERATION.
CC   -!- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF046874; AAC27249.1; -.
DR   HSSP; P20942; 1B9X.
DR   InterPro; IPR001200; Phosducin.
DR   InterPro; IPR006663; Thioredox_dom2.
DR   Pfam; PF02114; Phosducin; 1.
DR   PRINTS; PR00677; PHOSDUCIN.
KW   Vision; Sensory transduction; Phosphorylation; Disease mutation.
FT   MOD_RES      73     73       PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT   VARIANT      82     82       R -> G (IN PD).
SQ   SEQUENCE   245 AA;  28263 MW;  CFA3779E2B7DD236 CRC64;

  Query Match             61.8%;  Score 34;  DB 1;  Length 245;
  Best Local Similarity   75.0%;  Pred. No. 17;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TLRVYKGG 10
              || :|||
Db        188 TLLIYKGG 195


RESULT 14
PHOS_HUMAN
ID   PHOS_HUMAN     STANDARD;      PRT;   246 AA.
AC   P20941; Q14816;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein).
GN   PDC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pineal gland, and Retina;
RX   MEDLINE=91007277; PubMed=2210381;
RA   Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,
RA   Shinohara T.;
RT   "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in
RT   retina and pineal gland.";
RL   Gene 91:209-215(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90343823; PubMed=2383274;
```

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RA   Watanabe Y., Kawasaki K., Miki N., Kuo C.H.;
RT   "Isolation and analysis of the human MEKA gene encoding a retina-
RT   specific protein.";
RL   Biochem. Biophys. Res. Commun. 170:951-956(1990).
CC   -!- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
CC       PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
CC       METABOLISM.
CC   -!- SUBUNIT: Forms a complex with the beta and gamma subunits of
CC       the GTP-binding protein, transducin.
CC   -!- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
CC   -!- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
CC       MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
CC   -!- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
CC   -!- DATABASE: NAME=Mutations of the PDC gene;
CC       NOTE=Retina International's Scientific Newsletter;
CC       WWW="http://www.retina-international.com/sci-news/pdcmut.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M33478; AAA35486.1; -.
DR   EMBL; M38059; AAA36210.1; -.
DR   EMBL; M60720; AAA36210.1; JOINED.
DR   EMBL; M38058; AAA36210.1; JOINED.
DR   PIR; A35422; A35422.
DR   HSSP; P20942; 1B9X.
DR   Genew; HGNC:8759; PDC.
DR   MIM; 171490; -.
DR   GO; GO:0004859; F:phospholipase inhibitor activity; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0007602; P:phototransduction; TAS.
DR   InterPro; IPR001200; Phosducin.
DR   InterPro; IPR006663; Thioredox_dom2.
DR   Pfam; PF02114; Phosducin; 1.
DR   PRINTS; PR00677; PHOSDUCIN.
KW   Vision; Sensory transduction; Phosphorylation.
FT   MOD_RES      73     73       PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT   CONFLICT    140    140       I -> L (IN REF. 2).
SQ   SEQUENCE   246 AA;  28246 MW;  DF59C2C7C3308C90 CRC64;

  Query Match             61.8%;  Score 34;  DB 1;  Length 246;
  Best Local Similarity   75.0%;  Pred. No. 17;
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Qy          3 TLRVYKGG 10
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Db        188 TLLIYKGG 195


RESULT 15
APOH_HUMAN
ID   APOH_HUMAN     STANDARD;      PRT;   345 AA.
AC   P02749;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
DE   (Beta(2)GPI) (Activated protein C-binding protein) (APC inhibitor).
GN   APOH OR B2G1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=91315408; PubMed=1650181;
RA   Steinkasserer A., Estaller C., Weiss E., Sim R.B., Day A.J.;
RT   "Complete nucleotide and deduced amino acid sequence of human beta 2-
RT   glycoprotein I.";
RL   Biochem. J. 277:387-391(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=92008618; PubMed=1655523;
RA   Kristensen T., Schousboe I., Boel E., Mulvihill E.M., Hansen R.R.,
RA   Moeller K.B., Moeller N.P.H., Sottrup-Jensen L.;
RT   "Molecular cloning and mammalian expression of human beta
RT   2-glycoprotein I cDNA.";
RL   FEBS Lett. 289:183-186(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=92084151; PubMed=1748314;
RA   Mehdi H., Nunn M., Steel D.M., Whitehead A.S., Perez M., Walker L.,
RA   Peeples M.E.;
RT   "Nucleotide sequence and expression of the human gene encoding
RT   apolipoprotein H (beta 2-glycoprotein I).";
RL   Gene 108:293-298(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92273779; PubMed=1339416;
RA   Day J.R., O'Hara P.J., Grant F.J., Lofton-Day C.E., Berkaw M.N.,
RA   Werner P., Arnaud P.;
RT   "Molecular cloning and sequence analysis of the cDNA encoding human
RT   apolipoprotein H (beta 2-glycoprotein I).";
RL   Int. J. Clin. Lab. Res. 21:256-263(1992).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92135065; PubMed=1777418;
RA   Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
RA   Yasuda T., Koike T.;
RT   "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
RT   cDNA cloning and inter-species differences of beta 2-GPI in
RT   alternation of anticardiolipin binding.";
RL   Int. Immunol. 3:1217-1221(1991).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99115472; PubMed=9914524;
RA   Okkels H., Rasmussen T.E., Sanghera D.K., Kamboh M.I., Kristensen T.;
RT   "Structure of the human beta2-glycoprotein I (apolipoprotein H)
RT   gene.";
RL   Eur. J. Biochem. 259:435-440(1999).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX   MEDLINE=84222015; PubMed=6587378;
RA   Lozier J., Takahashi N., Putnam F.W.;
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RT   "Complete amino acid sequence of human plasma beta 2-glycoprotein I.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).
RN   [9]
RP   SEQUENCE OF 20-38.
RC   TISSUE=Follicular fluid;
RX   MEDLINE=21148139; PubMed=11250549;
RA   Aleporou-Marinou V., Pappa H., Yalouris P., Patargias T.;
RT   "Purification of apolipoprotein H (beta 2-glycoprotein I)-like protein
RT   from human follicular fluid.";
RL   Comp. Biochem. Physiol. 128B:537-542(2001).
RN   [10]
RP   DISULFIDE BONDS IN C-TERMINAL DOMAIN.
RX   MEDLINE=93050249; PubMed=1426288;
RA   Steinkkasserer A., Barlow P.N., Willis A.C., Kertesz Z.,
RA   Campbell I.D., Sim R.B., Norman D.G.;
RT   "Activity, disulphide mapping and structural modelling of the fifth
RT   domain of human beta 2-glycoprotein I.";
RL   FEBS Lett. 313:193-197(1992).
RN   [11]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE=97299942; PubMed=9155091;
RA   Gambino R., Ruiu G., Pagano G., Cassader M.;
RT   "Qualitative analysis of the carbohydrate composition of
RT   apolipoprotein H.";
RL   J. Protein Chem. 16:205-212(1997).
RN   [12]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RC   TISSUE=Plasma;
RX   MEDLINE=99437994; PubMed=10508150;
RA   Bouma B., de Groot P.G., van Den Elsen J.M.H., Ravelli R.B.G.,
RA   Schouten A., Simmelink M.J.A., Derksen R.H.W.M., Kroon J., Gros P.;
RT   "Adhesion mechanism of human beta(2)-glycoprotein I to phospholipids
RT   based on its crystal structure.";
RL   EMBO J. 18:5166-5174(1999).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.87 ANGSTROMS).
RX   MEDLINE=20031634; PubMed=10562535;
RA   Schwarzenbacher R., Zeth K., Diederichs K., Gries A., Kostner G.M.,
RA   Laggner P., Prassl R.;
RT   "Crystal structure of human beta2-glycoprotein I: implications for
RT   phospholipid binding and the antiphospholipid syndrome.";
RL   EMBO J. 18:6228-6239(1999).
RN   [14]
RP   VARIANT LEU-266.
RX   MEDLINE=93273313; PubMed=8099061;
RA   Steinkasserer A., Doerner C., Wuerzner R., Sim R.B.;
RT   "Human beta 2-glycoprotein I: molecular analysis of DNA and amino
RT   acid polymorphism.";
RL   Hum. Genet. 91:401-402(1993).
RN   [15]
RP   VARIANT ASN-107.
RX   MEDLINE=97369481; PubMed=9225969;
RA   Sanghera D.K., Kristensen T., Hamman R.F., Kamboh M.I.;
RT   "Molecular basis of the apolipoprotein H (beta 2-glycoprotein I)
RT   protein polymorphism.";
RL   Hum. Genet. 100:57-62(1997).
RN   [16]
RP   VARIANTS GLY-325 AND SER-335.
RX   MEDLINE=97217791; PubMed=9063752;
RA   Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.;
RT   "Identification of structural mutations in the fifth domain of
RT   apolipoprotein H (beta-2-glycoprotein I) which affect phospholipid
RT   binding.";
RL   Hum. Mol. Genet. 6:311-316(1997).
CC   -!- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
CC       SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
CC       ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
CC       TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC   -!- SIMILARITY: Contains 4 Sushi (SCR) domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   ---------------------------------------------------------------------
DR   EMBL; X58100; CAA41113.1; -.
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DR   EMBL; M62839; AAA51766.1; -.
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DR   EMBL; Y11494; CAA72279.1; JOINED.
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DR   EMBL; Y11496; CAA72279.1; JOINED.
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DR   PDB; 1C1Z; 19-NOV-99.
DR   PDB; 1G4F; 28-MAR-01.
DR   PDB; 1G4G; 28-MAR-01.
DR   Genew; HGNC:616; APOH.
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DR   Pfam; PF00084; sushi; 4.
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KW   Polymorphism; 3D-structure.
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FT   CHAIN        20    345       BETA-2-GLYCOPROTEIN I.
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